

STIC-Biotech/ChemLib

168351

ME

From: Myers, Carla
Sent: Wednesday, October 12, 2005 7:00 AM
To: STIC-Biotech/ChemLib
Subject: sequence search 09/887941

Please do an oligomer search in commercial and interference files for fragments of SEQ ID NO: **11 and 12**
- please limit the search results to nucleic acids of a length of 50 nucleotides or less.

Please provide a printout of the first 40 results.

The CRF has been entered; http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=09887941

Thank you

Carla Myers
AU 1634
Remsen Bldg / Rm 2E79
Mailbox: REM 2C70
571-272-0747

RECEIVED
OCT 12 2005
STIC/BIOTECH/CHM LIB
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 10/12/05
Date completed: 10/12/05
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# 2 AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: DSH
WWW/Internet: _____
Other (Specify): _____

RESULT 2
LOCUS AU107207/c 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU107207 Sugano Homo sapiens cDNA library Homo sapiens CDNA clone
ACCESSION HRC12745, mRNA sequence.
VERSION AU107207
KEYWORDS AU107207.1 GI:13556728
SOURCE EST. 1 to 50
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hara,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
149-156 (1997).
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Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 45 GCGGACGAGCAGA 32
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DEFINITION AU107210 Sugano Homo sapiens cDNA library Homo sapiens CDNA clone
ACCESSION KAT06101, mRNA sequence.
VERSION AU107210
KEYWORDS AU107210.1 GI:13556731
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hara,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
149-156 (1997).
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/clone_lib="Sugano Homo sapiens CDNA library"
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Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 49 GCGGACGAGCAGA 36
RESULT 4
LOCUS AU107211/c 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU107211 Sugano Homo sapiens cDNA library Homo sapiens CDNA clone
ACCESSION LNG05636, mRNA sequence.
VERSION AU107211
KEYWORDS AU107211.1 GI:13556732
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hara,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
149-156 (1997).
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG05636"
/clone_lib="Sugano Homo sapiens CDNA library"
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Query Match 7.1%; Score 14; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 152 GCGGACGAGCAGA 165
DB 43 GCGGACGAGCAGA 30
RESULT 5

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2005, 12:40:34 ; Search time 402.837 Seconds
(without alignments)
3410.666 Million cell updates/sec

Title: US-09-887-941B-12

Perfect score: 196

Sequence: 1 gggcgagcagcgaggaatca.....ttgagacggaggaagcact 196

Scoring table:

OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 8765912 seqs, 3504951483 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11015406

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

- Published Applications NA:*
- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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 - 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
 - 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
 - 22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq:*
 - 23: /cgn2_6/ptodata/2/pubpna/US10K_PUBCOMB.seq:*
 - 24: /cgn2_6/ptodata/2/pubpna/US10L_PUBCOMB.seq:*
 - 25: /cgn2_6/ptodata/2/pubpna/US10M_PUBCOMB.seq:*
 - 26: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 27: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 15 | 7.7 | 25 | US-10-098-263B-17480 |
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| 4 | 15 | 7.7 | 25 | US-10-098-263B-17480 |
| 5 | 15 | 7.7 | 25 | US-10-098-263B-17480 |
| 6 | 15 | 7.7 | 25 | US-10-098-263B-17480 |
| 7 | 15 | 7.7 | 25 | US-10-098-263B-17480 |

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| 8 | 15 | 7.7 | 25 | US-11-036-317-202981 |
| 9 | 15 | 7.7 | 25 | US-11-036-317-257966 |
| 10 | 15 | 7.7 | 25 | US-11-036-317-308169 |
| 11 | 15 | 7.7 | 25 | US-11-036-317-339642 |
| 12 | 15 | 7.7 | 25 | US-11-036-317-363827 |
| 13 | 15 | 7.7 | 25 | US-11-036-317-452734 |
| 14 | 15 | 7.7 | 25 | US-11-036-317-4890910 |
| 15 | 15 | 7.7 | 25 | US-11-036-317-927360 |
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| 17 | 15 | 7.7 | 25 | US-11-036-317-927360 |
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| 19 | 15 | 7.7 | 25 | US-11-036-317-927360 |
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| 36 | 15 | 7.7 | 25 | US-11-036-317-927360 |
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| 38 | 15 | 7.7 | 25 | US-11-036-317-927360 |
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ALIGNMENTS

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Sequence 17480, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 13106
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 17480
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-17480

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RESULT 2

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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 56424
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-56424

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DB 25 CCCGGAACCTCAGA 11

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; Sequence 195425, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-195425

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20050026164A1
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; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 489771
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; TYPE: DNA
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US-10-719-900-489771

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; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 CAGAGAGCGAGGCTG 115
DB 8 CAGAGAGCGAGGCTG 22

RESULT 6
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 180263
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; TYPE: DNA
; ORGANISM: Rattus norvegicus
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QY 97 ACCTCAGAGAGCGAG 111
DB 23 ACCTCAGAGAGCGAG 9

RESULT 7
US-10-719-956-315460
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2005, 09:55:07 ; Search time 87.6346 Seconds
(without alignments)
3659.630 Million cell updates/sec

Title: US-09-887-941B-12

Perfect score: 196

Sequence: 1 999CGCAGCAGGAGGAGTCA.....CTGAGACCGGAGGAGCAGCT 196

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- Issued Patents NA:*
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 - 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
 - 6: /cgn2_6/ptodata/1/ina/backfillseq.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|-----------------------|--------------------|
| 1 | 14 | 7.1 | 19 | US-09-422-936-19 | Sequence 19, Appl |
| 2 | 14 | 7.1 | 24 | US-09-000-630C-17 | Sequence 17, Appl |
| 3 | 14 | 7.1 | 24 | US-08-862-730C-17 | Sequence 17, Appl |
| 4 | 14 | 7.1 | 25 | US-09-396-196G-23342 | Sequence 23342, A |
| 5 | 14 | 7.1 | 25 | US-09-396-196G-112506 | Sequence 112506, |
| 6 | 14 | 7.1 | 25 | US-09-396-196G-112507 | Sequence 112507, |
| 7 | 14 | 7.1 | 39 | US-09-325-256-28 | Sequence 28, Appl |
| 8 | 14 | 7.1 | 40 | US-08-117-083-5 | Sequence 5, Appl |
| 9 | 13 | 6.6 | 17 | US-09-866-108A-2615 | Sequence 2615, Ap |
| 10 | 13 | 6.6 | 17 | US-09-866-108A-2616 | Sequence 2616, Ap |
| 11 | 13 | 6.6 | 17 | US-09-866-108A-2617 | Sequence 2617, Ap |
| 12 | 13 | 6.6 | 17 | US-09-866-108A-2618 | Sequence 2618, Ap |
| 13 | 13 | 6.6 | 17 | US-09-866-108A-2619 | Sequence 2619, Ap |
| 14 | 13 | 6.6 | 18 | US-09-167-109-86 | Sequence 86, Appl |
| 15 | 13 | 6.6 | 18 | US-09-167-109-87 | Sequence 87, Appl |
| 16 | 13 | 6.6 | 18 | US-09-866-028-44 | Sequence 44, Appl |
| 17 | 13 | 6.6 | 18 | US-09-944-457-44 | Sequence 44, Appl |
| 18 | 13 | 6.6 | 18 | 5512667-2 | Patent No. 5512667 |
| 19 | 13 | 6.6 | 18 | 5512667-2 | Patent No. 5512667 |
| 20 | 13 | 6.6 | 19 | US-08-598-873-70 | Sequence 70, Appl |
| 21 | 13 | 6.6 | 19 | US-08-605-430-70 | Sequence 70, Appl |
| 22 | 13 | 6.6 | 19 | US-09-717-054-70 | Sequence 70, Appl |
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| 24 | 13 | 6.6 | 20 | US-09-387-341-223 | Sequence 223, Appl |
| 25 | 13 | 6.6 | 20 | US-09-761-116-26 | Sequence 26, Appl |
| 26 | 13 | 6.6 | 22 | US-09-549-872B-17 | Sequence 17, Appl |
| 27 | 13 | 6.6 | 25 | US-09-866-108A-5544 | Sequence 5544, Ap |

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| 28 | 13 | 6.6 | 25 | US-09-866-108A-5545 | Sequence 5545, Ap |
| 29 | 13 | 6.6 | 25 | US-09-866-108A-5546 | Sequence 5546, Ap |
| 30 | 13 | 6.6 | 25 | US-09-866-108A-5547 | Sequence 5547, Ap |
| 31 | 13 | 6.6 | 25 | US-09-866-108A-5548 | Sequence 5548, Ap |
| 32 | 13 | 6.6 | 25 | US-09-866-108A-5549 | Sequence 5549, Ap |
| 33 | 13 | 6.6 | 25 | US-09-866-108A-5550 | Sequence 5550, Ap |
| 34 | 13 | 6.6 | 25 | US-09-866-108A-5551 | Sequence 5551, Ap |
| 35 | 13 | 6.6 | 25 | US-09-866-108A-5552 | Sequence 5552, Ap |
| 36 | 13 | 6.6 | 25 | US-09-866-108A-5553 | Sequence 5553, Ap |
| 37 | 13 | 6.6 | 25 | US-09-866-108A-5554 | Sequence 5554, Ap |
| 38 | 13 | 6.6 | 25 | US-09-866-108A-5555 | Sequence 5555, Ap |
| 39 | 13 | 6.6 | 25 | US-09-866-108A-5556 | Sequence 5556, Ap |
| 40 | 13 | 6.6 | 25 | US-09-396-196G-8224 | Sequence 8224, Ap |
| 41 | 13 | 6.6 | 25 | US-09-396-196G-12058 | Sequence 12058, A |
| 42 | 13 | 6.6 | 25 | US-09-396-196G-46116 | Sequence 46116, A |
| 43 | 13 | 6.6 | 25 | US-09-396-196G-59077 | Sequence 59077, A |
| 44 | 13 | 6.6 | 25 | US-09-396-196G-59088 | Sequence 59088, A |
| 45 | 13 | 6.6 | 25 | US-09-396-196G-67675 | Sequence 67675, A |

ALIGNMENTS

RESULT 1
US-09-422-936-19
; Sequence 19, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-422-936-19

Query Match 7.1%; Score 14; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 AGCCCGGGGAGAG 131
Db 6 AGCCCGGGGAGAG 19

RESULT 2
US-09-000-630C-17/C
; Sequence 17, Application US/0900630C
; Patent No. 6018029
; GENERAL INFORMATION:
; APPLICANT: Fuller, Gerald M
; APPLICANT: Puentes, Nelson L.
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
; TITLE OF INVENTION: Antagonist
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Douglas C Murdock/ Bradley, Arant, Rose & White
; STREET: 2001 Park Place, Suite 1400

CITY: Birmingham
STATE: Alabama
COUNTRY: USA
ZIP: 35203-2736
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,630C
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,730
FILING DATE:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-09-000-630C-17

Query Match 7.1%; Score 14; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 GAGGCTGACAGGCC 122
|||||
Db 21 GAGGCTGACAGGCC 8

RESULT 3
US-08-862-730C-17/c
Sequence 17, Application US/08862730C
Patent No. 6063600
GENERAL INFORMATION:
APPLICANT: Fuller, Gerald M.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
TITLE OF INVENTION: Antagonist
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Douglas C Murdock/ Bradley, Arant, Rose & White
STREET: 2001 Park Place, Suite 1400
CITY: Birmingham
STATE: Alabama
COUNTRY: USA
ZIP: 35203-2736
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,730C
FILING DATE: 5/23/97
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-08-862-730C-17

Query Match 7.1%; Score 14; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 109 GAGGCTGACAGGCC 122
|||||

Db 21 GAGGCTGACAGGCC 8

RESULT 4
US-09-396-196G-23342/c
Sequence 23342, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23342
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-23342

Query Match 7.1%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 AGGCTGACAGGCC 123
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Db 16 AGGCTGACAGGCC 3

RESULT 5
US-09-396-196G-112506/c
Sequence 112506, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 112506
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-112506

Query Match 7.1%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 ACCAGCGACAGAG 161
|||||
Db 25 ACCAGCGACAGAG 12

RESULT 6
US-09-396-196G-112507/c
Sequence 112507, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2005, 14:08:48 ; Search time 268.558 Seconds
(without alignments)
4320.373 Million cell updates/sec

Title: US-09-887-941B-12

Perfect score: 196
Sequence: 1 gggcgagcagcgaggaatca.....ttgagaccggaagcgacct 196

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:

- 1: Geneseqn19808:*
- 2: Geneseqn19908:*
- 3: Geneseqn20008:*
- 4: Geneseqn20018:*
- 5: Geneseqn20028:*
- 6: Geneseqn20038:*
- 7: Geneseqn20048:*
- 8: Geneseqn20058:*
- 9: Geneseqn20068:*
- 10: Geneseqn20078:*
- 11: Geneseqn20088:*
- 12: Geneseqn20098:*
- 13: Geneseqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 15 | 7.7 | 25 | 9 | AC117489 Human mic |
| 2 | 15 | 7.7 | 33 | 6 | ABa01159 Human ztn |
| 3 | 15 | 7.7 | 38 | 6 | AAQ10273 Probe B(I |
| 4 | 15 | 7.7 | 41 | 6 | ABa01162 Human ztn |
| 5 | 15 | 7.7 | 41 | 6 | ABa01161 Human ztn |
| 6 | 15 | 7.7 | 45 | 12 | ADM34012 Human SCN |
| 7 | 15 | 7.7 | 48 | 12 | ADM34013 Human SCN |
| 8 | 14 | 7.1 | 19 | 2 | AAK58088 Human SCN |
| 9 | 14 | 7.1 | 20 | 6 | AB197219 Capture o |
| 10 | 14 | 7.1 | 20 | 12 | ADJ31930 Human ocp |
| 11 | 14 | 7.1 | 21 | 4 | AAH62255 SUC1A6 po |
| 12 | 14 | 7.1 | 24 | 2 | AAV94895 Human G P |
| 13 | 14 | 7.1 | 24 | 2 | AAV99965 Nucleotid |
| 14 | 14 | 7.1 | 24 | 6 | AB144783 Human GAB |
| 15 | 14 | 7.1 | 24 | 6 | AB191008 Capture o |
| 16 | 14 | 7.1 | 24 | 6 | AB191009 Capture o |
| 17 | 14 | 7.1 | 25 | 6 | AC124415 Human mic |
| 18 | 14 | 7.1 | 25 | 2 | AAQ29387 Human RGS |
| 19 | 14 | 7.1 | 25 | 2 | AAQ29387 Human RGS |
| 20 | 13 | 6.6 | 17 | 6 | ABN02626 Human GDM |

| | | | | | | |
|----|----|-----|----|----|----------|--------------------|
| 21 | 13 | 6.6 | 17 | 6 | ABN02624 | Abn02624 Human GDM |
| 22 | 13 | 6.6 | 17 | 6 | ABN02623 | Abn02623 Human GDM |
| 23 | 13 | 6.6 | 17 | 6 | ABN02625 | Abn02625 Human GDM |
| 24 | 13 | 6.6 | 17 | 6 | ABN02627 | Abn02627 Human GDM |
| 25 | 13 | 6.6 | 17 | 10 | ADD19411 | Add19411 Salmo sal |
| 26 | 13 | 6.6 | 17 | 13 | ACN65713 | ACN65713 Human GDM |
| 27 | 13 | 6.6 | 17 | 13 | ACN65715 | ACN65715 Human GDM |
| 28 | 13 | 6.6 | 17 | 13 | ACN65716 | ACN65716 Human GDM |
| 29 | 13 | 6.6 | 17 | 13 | ACN65714 | ACN65714 Human GDM |
| 30 | 13 | 6.6 | 17 | 13 | ACN65717 | ACN65717 Human GDM |
| 31 | 13 | 6.6 | 18 | 2 | AAQ22412 | Aaq22412 3'-acridi |
| 32 | 13 | 6.6 | 18 | 2 | AAK80084 | Aax80084 Human PRO |
| 33 | 13 | 6.6 | 18 | 3 | AAK58510 | Aac58510 Human PRO |
| 34 | 13 | 6.6 | 18 | 3 | AAK55575 | Aaa55575 TRAF3 ant |
| 35 | 13 | 6.6 | 18 | 3 | AAK55576 | Aaa55576 TRAF3 ant |
| 36 | 13 | 6.6 | 18 | 3 | AAQ01254 | Aad01254 Forward P |
| 37 | 13 | 6.6 | 18 | 3 | AAA49490 | Aaa49490 Primer fo |
| 38 | 13 | 6.6 | 18 | 3 | AAA49490 | Aaa49490 PCR prime |
| 39 | 13 | 6.6 | 18 | 8 | ABX96800 | Abx96800 Human PRO |
| 40 | 13 | 6.6 | 18 | 8 | ABX78454 | Abx78454 Novel hum |
| 41 | 13 | 6.6 | 18 | 8 | ABX77088 | Abx77088 Human PRO |
| 42 | 13 | 6.6 | 18 | 8 | ABX75919 | Abx75919 Human PRO |
| 43 | 13 | 6.6 | 18 | 8 | ABX89630 | Abx89630 Novel hum |
| 44 | 13 | 6.6 | 18 | 8 | ABX34116 | Abx34116 Human PRO |
| 45 | 13 | 6.6 | 18 | 9 | ACA04336 | ACA04336 Human PRO |

ALIGNMENTS

RESULT 1

ID AC117489 standard; DNA; 25 BP.

AC117489;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 17480.

XX EST, ss; probe; expressed sequence tag; microarray; gene expression;

XX genetic variation; diallelic marker; polymorphism; human;

XX cross-species comparison.

OS Homo sapiens.

PN US200310410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00096263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

PI Mittmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 17480; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis

CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 7.7%; Score 15; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 CAGGAACCTCAGAGA 106
 |||||
 DB 3 CAGGAACCTCAGAGA 17

RESULT 2
 ABA01159
 ID ABA01159 standard; DNA; 33 BP.

AC ABA01159;

XX 24-JAN-2002 (first entry)

DE Human zinc finger protein 72 PCR primer #3.

XX Human; zinc finger protein 72; cytosolic; virucidal; immunomodulatory;

KW antiinflammatory; haemostatic; anti-HIV; gene therapy; cancer;

KM haemopathy; HIV infection; immunological disease; inflammation;

XX nervous system disease; developmental disorder; PCR primer; se.

OS Homo sapiens.

XX WO200174866-A1.

XX 11-OCT-2001.

PF 26-FEB-2001; 2001WO-CN000196.

XX 02-MAR-2000; 2000CN-00111866.

XX (BIOW-) B10WINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-025795/03.

XX New human zinc finger protein 72 for diagnosing and treating malignant

XX tumor, hemopathy, human immunodeficiency virus infection, immunological

XX diseases and various inflammations.

XX Example 5; Page 13; 38pp; Chinese.

XX The present invention relates to human zinc finger protein 72 (see

XX AAM5332). The zinc finger protein and its coding sequence are useful in

XX the diagnosis and treatment of cancer, hemopathy, HIV infection,

XX immunological diseases, various inflammations, nervous system diseases

XX and developmental disorders. The present sequence is a PCR primer, which

XX was used in an example from the present invention

XX Sequence 33 BP; 9 A; 8 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 7.7%; Score 15; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 TGAGTCCAGGAACC 99
 |||||
 DB 15 TGAGTCCAGGAACC 29

RESULT 3
 AAQ10273
 ID AAQ10273 standard; DNA; 38 BP.

XX AAQ10273;

AC 25-MAR-2003 (revised)

XX 03-APR-1991 (first entry)

DE Probe B(II) for bovine BMP exon 3.

XX Bone morphogenetic protein; cartilage; antibodies; osteoporosis;

KW osteoarthritis; screening.

XX Synthetic.

XX EP409472-A.

XX 23-JAN-1991.

XX 11-JUL-1990; 90EP-00307568.

XX 19-JUL-1989; 89US-00382805.

XX (CHIR) CHIRON CORP.

XX Keifer MC, Maslarz FR, Barr PJ;

XX WPI; 1991-024045/04.

XX Purified mammalian bone morphogenetic protein - and recombinant DNA

XX encoding it, useful in pharmaceuticals for cartilage and bone formation.

XX Disclosure; Fig 1; 26pp; English.

XX The sequence is the complement of probe B designed to bind to a DNA

XX encoding tryptic peptide B, found in exon 3 of bovine BMP genomic DNA.

XX Recombinantly produced BMP can be used to induce cartilage and bone

XX formation in vertebrates (dose =ca. 0.1 ug-100mg/kg). Ads raised to the

XX CC protein may be used to inhibit or to reverse e.g. osteoporosis,

XX osteoarthritis, etc. Purified BMP will be partic. useful in the design

XX CC and screening of cartilage/bone growth inhib- itors. See also AAQ10265-

XX Q10276. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 BP; 7 A; 11 C; 11 G; 5 T; 0 U; 4 Other;

Query Match 7.7%; Score 15; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 GAGAGCGAGCTGAC 117
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 DB 1 GAGAGCGAGCTGAC 15

RESULT 4
 ABA01162
 ID ABA01162 standard; DNA; 41 BP.

XX ABA01162;

XX 24-JAN-2002 (first entry)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2005, 14:11:57 : Search time 1437.02 Seconds
(without alignments)
6608.974 Million cell updates/sec

Title: US-09-887-941B-12

Perfect score: 196
Sequence: 1 ggcgcgcacgcgagggagctca.....ctgagaccgggaagcact 196

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 14 | 7.1 | 19 | AR236573 | Sequence |
| 2 | 14 | 7.1 | 20 | AX297177 | Sequence |
| 3 | 14 | 7.1 | 24 | E13893 | PCR primer |
| 4 | 14 | 7.1 | 24 | AX292544 | Sequence |
| 5 | 14 | 7.1 | 24 | AX318212 | Sequence |
| 6 | 14 | 7.1 | 25 | AX815614 | Sequence |
| 7 | 14 | 7.1 | 39 | AR226526 | Sequence |
| 8 | 14 | 7.1 | 40 | I88811 | Sequence |
| 9 | 14 | 7.1 | 49 | MUSJHCD6 | Sequence |
| 10 | 13 | 6.6 | 17 | CO617875 | Sequence |
| 11 | 13 | 6.6 | 17 | CO617876 | Sequence |
| 12 | 13 | 6.6 | 17 | CO617877 | Sequence |
| 13 | 13 | 6.6 | 17 | CO617878 | Sequence |
| 14 | 13 | 6.6 | 17 | CO617879 | Sequence |
| 15 | 13 | 6.6 | 17 | AR458938 | Sequence |
| 16 | 13 | 6.6 | 17 | AR458939 | Sequence |
| 17 | 13 | 6.6 | 17 | AR458940 | Sequence |
| 18 | 13 | 6.6 | 17 | AR458941 | Sequence |
| 19 | 13 | 6.6 | 17 | AR458942 | Sequence |

| | | | | | | |
|------|----|-----|----|---|----------|-----------|
| C 20 | 13 | 6.6 | 17 | 6 | AX803878 | Sequence |
| C 21 | 13 | 6.6 | 18 | 6 | BD140553 | Polypepti |
| C 22 | 13 | 6.6 | 18 | 6 | BD224951 | Antisense |
| C 23 | 13 | 6.6 | 18 | 6 | BD224952 | Antisense |
| C 24 | 13 | 6.6 | 18 | 6 | BD264357 | Methods a |
| C 25 | 13 | 6.6 | 18 | 6 | AR211173 | Sequence |
| C 26 | 13 | 6.6 | 18 | 6 | AR211174 | Sequence |
| C 27 | 13 | 6.6 | 18 | 6 | AR365580 | Sequence |
| C 28 | 13 | 6.6 | 18 | 6 | AR429072 | Sequence |
| C 29 | 13 | 6.6 | 18 | 6 | AR534963 | Sequence |
| C 30 | 13 | 6.6 | 19 | 6 | AR156414 | Sequence |
| C 31 | 13 | 6.6 | 19 | 6 | CQ790275 | Sequence |
| C 32 | 13 | 6.6 | 20 | 6 | AR137950 | Sequence |
| C 33 | 13 | 6.6 | 20 | 6 | BD265675 | Transcrip |
| C 34 | 13 | 6.6 | 20 | 6 | CQ871039 | Sequence |
| C 35 | 13 | 6.6 | 20 | 6 | AR215675 | Sequence |
| C 36 | 13 | 6.6 | 20 | 6 | AR559926 | Sequence |
| C 37 | 13 | 6.6 | 20 | 6 | AX286799 | Sequence |
| C 38 | 13 | 6.6 | 20 | 6 | AX295275 | Sequence |
| C 39 | 13 | 6.6 | 20 | 6 | AX955684 | Sequence |
| C 40 | 13 | 6.6 | 20 | 6 | AX955736 | Sequence |
| C 41 | 13 | 6.6 | 21 | 6 | BD251425 | Ion chan |
| C 42 | 13 | 6.6 | 21 | 6 | AX023789 | Sequence |
| C 43 | 13 | 6.6 | 21 | 6 | AX803879 | Sequence |
| C 44 | 13 | 6.6 | 22 | 6 | BD247913 | Method fo |
| C 45 | 13 | 6.6 | 22 | 6 | AR302009 | Sequence |

ALIGNMENTS

RESULT 1
LOCUS AR236573 19 bp DNA
DEFINITION Sequence 19 from patent US 6465213.
ACCESSION AR236573
VERSION AR236573.1 GI:27280642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ekstrand,J.
TITLE Nucleotide sequences
JOURNAL Parent: US 6465213-A 19 15-OCT-2002;
FEATURES
source location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 7.1%; Score 14; DB 6; Length 19;
Best local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 118 AGGCCCGGCGAGAG 131
DB 6 AGGCCCGGCGAGAG 19

RESULT 2

LOCUS AX297177 20 bp DNA
DEFINITION Sequence 8939 from Patent WO0179548.
ACCESSION AX297177
VERSION AX297177.1 GI:17058868
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Barany,F., Zhiry,M., Gerry,N.P., Favis,R. and Kilman,R.
TITLE Method of designing addressable array for detection of nucleic acid

sequence differences using ligase detection reaction
Patent: WO 0179548-A 8939 25-OCT-2001;
CORNBEL RESEARCH FOUNDATION, INC. (US)

JOURNAL
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN
Query Match 7.1%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26 GAGCCCGAAGATGG 39
DB 4 GAGCCCGAAGATGG 17
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RESULT 3
LOCUS E13893 24 bp DNA linear PAT 27-APR-1998
DEFINITION PCR primer for gaining human G protein-coupling receptor gene.
ACCESSION E13893
VERSION E13893.1 GI:3252660
KEYWORDS JP 1997238686-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,K. and Fujii,A.
TITLE NEW G-PROTEIN COUPLED TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND
JOURNAL Patent: JP 1997238686-A 2 16-SEP-1997;
TAKEDA CHEM IND LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1997238686-A/2
PD 16-SEP-1997
PF 07-MAR-1996 JP 1996050678
PI HINUMA KUNIJU, FUJII AKIRA
PC C12N15/09,A61K48/00,C07H21/04,C12N1/21,C12P21/02,C12P21/08, PC
C12Q1/02,
PC G01N33/566//A61K39/395,(C12N1/21,C12R1.19),(C12P21/02, PC
C12R1.19),(C12P21/08,
PC C12R1.91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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LOCATION/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 GATGAGTCCCGAGA 96
DB 17 GATGAGTCCCGAGA 4
|||||

RESULT 4
LOCUS AX292544 24 bp DNA linear PAT 21-NOV-2001
AX292544

DEFINITION Sequence 4306 from Patent W00179548.
ACCESSION AX292544
VERSION AX292544.1 GI:17054227
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Barany,F., Zilvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL Sequence differences using ligase detection reaction
Patent: WO 0179548-A 4306 25-OCT-2001;
CORNBEL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN
Query Match 7.1%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26 GAGCCCGAAGATGG 39
DB 4 GAGCCCGAAGATGG 17
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RESULT 5
LOCUS AX318212 24 bp DNA linear PAT 14-DEC-2001
AX318212
DEFINITION Sequence 13 from Patent W00190163.
ACCESSION AX318212
VERSION AX318212.1 GI:17900895
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Ng,G.Y.
TITLE Use of the gaba b? receptor in assays to identify gamma
hydroxybutyrate agonists, antagonists, and allosteric modulators of
agonists
JOURNAL Patent: WO 0190163-A 13 29-NOV-2001;
Merck Frosst Canada & Co. (CA)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

ORIGIN
Query Match 7.1%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 AGGCCCGGAGAG 131
DB 3 AGGCCCGGAGAG 16
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RESULT 6
LOCUS AX815614 25 bp DNA linear PAT 09-DEC-2003
AX815614
DEFINITION Sequence 12 from Patent W003066904.
ACCESSION AX815614
VERSION AX815614.1 GI:39646311
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2005, 15:23:04 ; Search time 1905.96 Seconds
(without alignments)
4393.656 Million cell updates/sec

Title: US-09-887-941B-11

Perfect score: 220
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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2: gb_est2:*
3: gb_hc3:*
4: gb_est3:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 14 | 6.4 | 23 | 1 | AB094450 AB094450 |
| 3 | 14 | 6.4 | 28 | 9 | CG722869 1119073G0 |
| 4 | 14 | 6.4 | 29 | 8 | BH755587 SALK_0518 |
| 5 | 14 | 6.4 | 31 | 1 | AU732952 AU732952 |
| 6 | 14 | 6.4 | 45 | 9 | CL658678 PRI0132A |
| 7 | 14 | 6.4 | 47 | 7 | CF310621 ABE--05-F |
| 8 | 14 | 6.4 | 47 | 8 | AZ513870 1M0360X08 |
| 9 | 14 | 6.4 | 49 | 9 | CU529376 HTY40G02. |
| 10 | 14 | 6.4 | 50 | 1 | AU102598 AU102598 |
| 11 | 14 | 6.4 | 50 | 1 | AU107543 AU107543 |
| 12 | 14 | 6.4 | 50 | 9 | BX288916 Arabidops |
| 13 | 14 | 6.4 | 50 | 9 | CG710737 1119018F0 |
| 14 | 13 | 5.9 | 19 | 7 | CF324209 HDN--05-O |
| 15 | 13 | 5.9 | 26 | 8 | AZ454352 1M0256G18 |
| 16 | 13 | 5.9 | 29 | 1 | AZ582689 1M0376D13 |
| 17 | 13 | 5.9 | 29 | 1 | AU256240 AU256240 |
| 18 | 13 | 5.9 | 29 | 7 | N22525 |
| 19 | 13 | 5.9 | 29 | 8 | AZ356943 1M0098D16 |
| 20 | 13 | 5.9 | 32 | 8 | AZ288692 2M0105N15 |
| 21 | 13 | 5.9 | 32 | 8 | AZ408275 1M0179G20 |
| 22 | 13 | 5.9 | 32 | 9 | BK656232 Arabidops |
| 23 | 13 | 5.9 | 33 | 7 | CF307411 HDX1--06- |
| 24 | 13 | 5.9 | 36 | 5 | BQ035387 SK2-0117 |

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|-----|----|-----|----|---|----------|--------------------|
| 25. | 13 | 5.9 | 43 | 8 | AZ830331 | AZ830331 2M0109H03 |
| 26 | 13 | 5.9 | 43 | 8 | AZ877472 | AZ877472 2M0192L19 |
| 27 | 13 | 5.9 | 46 | 1 | A1631069 | A1631069 t232b10.x |
| 28 | 13 | 5.9 | 46 | 8 | CC178512 | CC178512 NPX329_Ba |
| 29 | 13 | 5.9 | 47 | 9 | AZ420561 | AZ420561 1M0198021 |
| 30 | 13 | 5.9 | 47 | 9 | AJ591522 | AJ591522 Arabidops |
| 31 | 13 | 5.9 | 48 | 8 | BH901106 | BH901106 KG09864-5 |
| 32 | 13 | 5.9 | 49 | 8 | AZ642798 | AZ642798 1M0506D02 |
| 33 | 13 | 5.9 | 49 | 9 | CR356331 | CR356331 Arabidops |
| 34 | 13 | 5.9 | 50 | 1 | AU104216 | AU104216 AU104216 |
| 35 | 13 | 5.9 | 50 | 1 | AU104712 | AU104712 AU104712 |
| 36 | 13 | 5.9 | 50 | 1 | AU107973 | AU107973 AU107973 |
| 37 | 13 | 5.9 | 50 | 9 | AJ591492 | AJ591492 Arabidops |
| 38 | 13 | 5.9 | 50 | 9 | AL943250 | AL943250 Arabidops |
| 39 | 12 | 5.5 | 20 | 8 | AZ490328 | AZ490328 1M0323A18 |
| 40 | 12 | 5.5 | 25 | 1 | A1539240 | A1539240 tp64b08.x |
| 41 | 12 | 5.5 | 25 | 8 | AZ635993 | AZ635993 1M0493520 |
| 42 | 12 | 5.5 | 25 | 8 | B2762357 | B2762357 SALK_1003 |
| 43 | 12 | 5.5 | 31 | 8 | AZ336296 | AZ336296 1M0066F01 |
| 44 | 12 | 5.5 | 31 | 8 | AZ763536 | AZ763536 1M0559I02 |
| 45 | 12 | 5.5 | 31 | 9 | CG707251 | CG707251 1119001G0 |

ALIGNMENTS

RESULT 1
CL437571 40 bp DNA linear GSS 18-MAR-2004

LOCUS PST5874-NL.Seg MICB1 Mus musculus genomic clone PST5874-NL.Seg,
DEFINITION genomic survey sequence.
ACCESSION CL437571
VERSION CL437571.1 GI:45573360
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 40)
Hicks, G.G.
TITLE www.BScellib.ca
JOURNAL Unpublished (2002)
COMMENT Contact: Hicks GG

Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190

Email: hicksgg@cc.umanitoba.ca
U3NeosVI gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST5874-NL.Se

Class: Gene Trap.
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST5874-NL.Seg"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosVI"

FEATURES

source

ORIGIN

Query Match 7.3%; Score 16; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 CCGGATTCGCAAGT 182
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 Db 8 CCGGATTCGCAAGT 23

RESULT 2

AB094450/c 23 bp mRNA linear EST 01-MAY-2003
 LOCUS AB094450 lambda Triplex2 rice phloem sap cDNA Oryza sativa
 DEFINITION (japonica cultivar-group) cDNA clone PA158, mRNA sequence.
 ACCESSION AB094450
 VERSION AB094450.1 GI:30307355
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 23)

AUTHORS Mano,H., Noguchi,M., Oshima,T., Yoneyama,T., Hayashi,H. and
 Fujikawa,T.
 TITLE Small RNAs detected in the rice phloem sap
 JOURNAL Unpublished (2003)
 COMMENT Contact: Hiromori Mano
 Plant Genome Center Co.,Ltd
 Kamondai-1-25-2, Tsukuba, Ibaraki 305-0856, Japan
 Tel: 81-298-39-4823
 Email: hmano@pccn.co.jp.

FEATURES

source Location/Qualifiers

1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="PA158"
 /tissue_type="phloem"
 /clone_id="lambda Triplex2 rice phloem sap cDNA"

ORIGIN

Query Match 6.4%; Score 14; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 TTTCCTCTCCTC 38
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 Db 20 TTTCCTCTCCTC 7

RESULT 3
 CG722869 28 bp DNA linear GSS 20-OCT-2003
 LOCUS 1119073G09.1EB_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
 DEFINITION survey sequence.
 ACCESSION CG722869
 VERSION CG722869.1 GI:37758149
 KEYWORDS GSS.

SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 28)

AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1119073 row: G column: 09
 Class: transposon-tagged.
 Location/Qualifiers

1..28
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A18/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_id="1119 - RescueMu Grid AA"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'RescueMu', 'Grid AA was grown at UC San Diego in 2002. DNA
 was extracted from leaf strips, double digested using
 BamHI and BglII, and ligated to form circular plasmids.
 DH10B cells were transformed and then screened on LB
 plates with ampicillin."

ORIGIN

Query Match 6.4%; Score 14; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CTTTCCCTTCC 29
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 Db 3 CTTTCCCTTCC 16

RESULT 4
 BH755587 29 bp DNA linear GSS 01-MAR-2002
 LOCUS SALK_051892.52.10 x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_051892.52.10.x, genomic
 survey sequence.
 ACCESSION BH755587
 VERSION BH755587.1 GI:19035884
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Viridiplantae; Spermatophyta; core eudicots;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosoids; eurosoids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 29)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 TITLE A sequence-indexed library of insertion mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 At2g38080.
 Class: TDNA tagged.
 Location/Qualifiers

1..29
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"


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; Sequence 616433, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 616433
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-616433

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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      152 GGCCGTGCGACATTTCCGAATTCT 176
Db      1 GGCCGTGCGACATTTCCGAATTCT 25

RESULT 3
US-10-719-900-654770
; Sequence 654770, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 654770
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-654770

Query Match      11.4%; Score 25; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      76 GGTCCTTTGTCAACGGCGGCCAC 100
Db      1 GGTCCTTTGTCAACGGCGGCCAC 25

RESULT 4
US-10-719-900-717050
; Sequence 717050, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 717050
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-717050

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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      77 GTGCTTTGTCAACGGCGGCCACT 101
Db      1 GTGCTTTGTCAACGGCGGCCACT 25

RESULT 5
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; Sequence 958924, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 958924
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-958924

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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      83 TTGTCAACGGCGGCCACTGCCGA 107
Db      1 TTGTCAACGGCGGCCACTGCCGA 25

RESULT 6
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; Sequence 20600, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 20600
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-20600

Query Match      11.4%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      150 CCGCGGTGCGACATTTCCGAATT 174
Db      1 CCGCGGTGCGACATTTCCGAATT 25

RESULT 7
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2005, 09:55:07 ; Search time 98.1654 Seconds
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3659.630 Million cell updates/sec

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Searched: 1202784 seqs, 818138359 residues

Word size : 0

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Maximum DB seq length: 50

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 3 | 20 | 9.1 | 40 | 2 | US-08-857-946-150 |
| 4 | 20 | 9.1 | 40 | 3 | US-08-970-740-150 |
| 5 | 16 | 7.3 | 34 | 1 | US-08-413-813-41 |
| 6 | 16 | 7.3 | 34 | 2 | US-08-467-346-41 |
| 7 | 15 | 6.8 | 20 | 3 | US-08-275-951-39 |
| 8 | 15 | 6.8 | 31 | 3 | US-08-848-373-1 |
| 9 | 15 | 6.8 | 36 | 1 | US-08-370-567-30 |
| 10 | 15 | 6.8 | 36 | 1 | US-08-438-759-30 |
| 11 | 15 | 6.8 | 36 | 1 | US-08-538-911-5 |
| 12 | 15 | 6.8 | 36 | 1 | US-08-117-361C-17 |
| 13 | 15 | 6.8 | 36 | 5 | PCT-US94-05591-5 |
| 14 | 15 | 6.8 | 36 | 5 | PCT-US94-05684-30 |
| 15 | 14 | 6.4 | 20 | 3 | US-09-357-073-12 |
| 16 | 14 | 6.4 | 20 | 3 | US-09-357-073-13 |
| 17 | 14 | 6.4 | 20 | 3 | US-09-357-073-14 |
| 18 | 14 | 6.4 | 20 | 3 | US-09-357-073-15 |
| 19 | 14 | 6.4 | 25 | 4 | US-09-396-196G-2778 |
| 20 | 14 | 6.4 | 25 | 4 | US-09-396-196G-25595 |
| 21 | 14 | 6.4 | 25 | 4 | US-09-396-196G-66126 |
| 22 | 14 | 6.4 | 25 | 4 | US-09-396-196G-66137 |
| 23 | 14 | 6.4 | 27 | 3 | US-09-253-396A-59 |
| 24 | 14 | 6.4 | 29 | 1 | US-08-342-411A-32 |
| 25 | 14 | 6.4 | 29 | 5 | PCT-US94-12883-32 |
| 26 | 14 | 6.4 | 30 | 3 | US-07-861-458C-61 |
| 27 | 14 | 6.4 | 33 | 1 | US-08-036-555B-90 |

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| 28 | 14 | 6.4 | 33 | 1 | US-08-036-555B-93 | Sequence 93, Appl |
| 29 | 14 | 6.4 | 33 | 1 | US-08-469-569-90 | Sequence 90, Appl |
| 30 | 14 | 6.4 | 33 | 1 | US-08-469-569-93 | Sequence 93, Appl |
| 31 | 14 | 6.4 | 33 | 1 | US-08-249-322A-90 | Sequence 90, Appl |
| 32 | 14 | 6.4 | 33 | 1 | US-08-249-322A-93 | Sequence 93, Appl |
| 33 | 14 | 6.4 | 33 | 1 | US-08-469-526A-90 | Sequence 90, Appl |
| 34 | 14 | 6.4 | 33 | 1 | US-08-469-526A-93 | Sequence 93, Appl |
| 35 | 14 | 6.4 | 33 | 2 | US-08-734-591A-90 | Sequence 90, Appl |
| 36 | 14 | 6.4 | 33 | 2 | US-08-734-591A-93 | Sequence 93, Appl |
| 37 | 14 | 6.4 | 33 | 2 | US-08-469-660-90 | Sequence 90, Appl |
| 38 | 14 | 6.4 | 33 | 2 | US-08-469-660-93 | Sequence 93, Appl |
| 39 | 14 | 6.4 | 33 | 2 | US-08-671-978A-16 | Sequence 16, Appl |
| 40 | 14 | 6.4 | 33 | 3 | US-08-470-335-90 | Sequence 90, Appl |
| 41 | 14 | 6.4 | 33 | 3 | US-08-470-335-93 | Sequence 93, Appl |
| 42 | 14 | 6.4 | 33 | 3 | US-08-735-021-90 | Sequence 90, Appl |
| 43 | 14 | 6.4 | 33 | 3 | US-08-735-021-93 | Sequence 93, Appl |
| 44 | 14 | 6.4 | 33 | 3 | US-08-734-664A-90 | Sequence 90, Appl |
| 45 | 14 | 6.4 | 33 | 3 | US-08-734-664A-93 | Sequence 93, Appl |

ALIGNMENTS

RESULT 1
US-08-857-946-149
Sequence 149, Application US/08857946
Patent No. 5994075
GENERAL INFORMATION:
APPLICANT: Goodfellow, P.N.
TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A
TITLE OF INVENTION: GENE OF INTEREST
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Witcoff, Inc.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,946
FILING DATE: 16-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/017,824
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3529/05573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: primer Pax6Mm12f
US-08-857-946-149

Query Match 9.1%, Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 GTCACAGCGAGTGAATCAG 69
|||||
Db 19 GTCACAGCGAGTGAATCAG 38

RESULT 2

US-08-970-740-149
; Sequence 149, Application US/08970740
; Patent No. 6015670
; GENERAL INFORMATION:
; APPLICANT: Goodfellow, P.N.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A
; TITLE OF INVENTION: GENE OF INTEREST
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Inc.
; STREET: 28 State Street, 28th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,740
; FILING DATE: 14-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/857,946
; FILING DATE: 16-MAY-1997
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 60/017,824
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathleen M. Williams
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3529/59829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-7111
; TELEFAX: 617-227-4399
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: primer Pax6mm121f
US-08-970-740-149

Query Match 9.1%; Score 20; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 GTCACAGCGAGTGAATCAG 69
|||||
Db 19 GTCACAGCGAGTGAATCAG 38

RESULT 3

US-08-857-946-150/c
; Sequence 150, Application US/08857946
; Patent No. 5994075
; GENERAL INFORMATION:
; APPLICANT: Goodfellow, P.N.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A
; TITLE OF INVENTION: GENE OF INTEREST
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Inc.

STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/857,946
FILING DATE: 16-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/60/017,824
FILING DATE: 17-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3529/05573

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

FEATURE:

NAME/KEY: primer Pax6mm121r

US-08-857-946-150
Query Match 9.1%; Score 20; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 160 GACATTTCCCGAATTCGCA 179
|||||
Db 40 GACATTTCCCGAATTCGCA 21

RESULT 4

US-08-970-740-150/c
; Sequence 150, Application US/08970740
; Patent No. 6015670
; GENERAL INFORMATION:
; APPLICANT: Goodfellow, P.N.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A
; TITLE OF INVENTION: GENE OF INTEREST
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Inc.
; STREET: 28 State Street, 28th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,740
; FILING DATE: 14-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/857,946
; FILING DATE: 16-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,824

CC to tissue-disruption to provide a mixed population (MP) comprising UC,
 CC subjecting MP to a cell size-discrimination (SD) step, and simultaneously
 CC or sequentially with SD, subjecting the cell population obtained to a
 CC cell-surface marker-discrimination step. Also described: (1) a
 CC substantially homogeneous population of undifferentiated cells (I)
 CC prepared by (M); (2) a composition (II) for use in cell replacement
 CC therapy, comprising a population of substantially homogeneous population
 CC of neural stem cells (NSCs) generated by (M); and (3) a composition (III)
 CC comprising a growth factor identified using a homogeneous population of
 CC NSCs generated by (M). (I) can have neurotropic, neuroprotective and
 CC antiapoptotic activities, and can be used in gene therapy. (M) is
 CC useful for generating a substantially homogeneous population of
 CC undifferentiated cells such as NSCs from a biological sample, and is
 CC useful for the replacement of neural or non-neural tissue in an animal.
 CC (II) is useful in cell replacement therapy in an organ such as the brain
 CC or in the nervous system, preferably central nervous system (CNS), for
 CC treating a CNS disorder such as Alzheimer's disease, Parkinson's disease,
 CC acute brain injury and CNS dysfunction. (I) is useful for the repair or
 CC regeneration of tissue. AB280278 to AB280363 represent PCR primers which
 CC are used in an example from the present invention for markers defining
 CC cell populations

XX Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 10.9%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred.No. 0.089;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 CTCACCGCGAGAGATTGTAGA 131
 |||||
 1 CTCACCGCGAGAGATTGTAGA 24

RESULT 2

AD007907
 ID AD007907 standard; DNA; 23 BP.

AC AD007907;

DT 07-OCT-2004 (first entry)

DE Sense primer for RT-PCR analysis of PAX6 gene.

XX Antidiabetic; human hepatic cell; insulin; FH-B-TPN; type 1; diabetes;

KM pancreatic duodenal homeobox gene-1; Pdx 1; insulin-dependent; PCR;

KM primer; ss.

XX Unidentified.

OS WO2004061091-A2.

PN 22-JUL-2004.

XX 05-JAN-2004; 2004WO-GB000005.

PR 06-JAN-2003; 2003GB-00000208.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

PI Efrat S;

XX WPI; 2004-534380/51.

PT New modified human hepatic cell, which is insulin-producing, useful as a

XX medicament for treating insulin-dependent diabetes.

XX Example; Fig 9; 46pp; English.

CC The invention relates to a modified human hepatic cell, which is insulin-
 CC producing. Further disclosed is an insulin-producing cell line designated
 CC FH-B-TPN, a method of making an insulin-producing cell line, a method of
 CC treatment of type 1 diabetes, a method of making insulin in-vitro, and a
 CC vector for the expression of pancreatic duodenal homeobox gene-1 (Pdx1),

CC where the vector is a lentiviral vector. The modified human hepatic cell
 CC is useful for treating insulin-dependent diabetes. Sequences given in
 CC records for AD007888-AD007961 represent primers for the RT-PCR analysis
 CC of RNA extracted from cultured cells, mature human hepatocytes, and human
 CC pancreatic islets.

XX Sequence 23 BP; 7 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 9.5%; Score 21; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred.No. 2.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GTCACAGCGAGTGAATCAGC 70
 |||||
 3 GTCACAGCGAGTGAATCAGC 23

Db 3 GTCACAGCGAGTGAATCAGC 23
 |||||
 3 GTCACAGCGAGTGAATCAGC 23

AC AAV16077;

DT 21-MAY-1998 (first entry)

DE PCR primer used to identify PAX6 mutations in mice.

XX Mutation; mutational screening; recessive; phenotypic alteration;

KW single strand conformation polymorphism; SSCP; PAX6 gene; aniridia;

KM PCR primer; amplify; ss.

XX Synthetic.

OS Mus sp.

PN WO9744485-A1.

XX 27-NOV-1997.

XX 16-MAY-1997; 97WO-GB001354.

PR 17-MAY-1996; 96GB-00010355.

XX (HEXA-) HEXAGEN TECHNOLOGY LTD.

PI Goodfellow PN;

XX WPI; 1998-018536/02.

PT Identification of mutation(s) in genes of interest - without prior

XX observation of phenotypic alteration in the mutated organism or cell.

XX Example 11; Page 58; 66pp; English.

CC PCR primers AAV16059-76 were used to identify PAX6 mutations in mice
 CC using the method of the invention. The method comprises testing a nucleic
 CC acid sample from a mutated organism for a mutation in a gene of interest
 CC without the prior observation of a phenotypic alteration in the mutated
 CC organism resulting from the mutation. PAX6 mutations lead to a variety of
 CC anterior segment malformations most commonly characterised by eye
 CC development defects broadly described as aniridia. The disease is
 CC dominant. A population of male mice were treated with ENVU to provide a
 CC source of mutant PAX6 and a heterozygotic F1 generation produced.
 CC Fluorescent single strand conformation polymorphism (SSCP) is utilised to
 CC identify those members of the F1 population carrying PAX6 mutations. The
 CC method provides mutational screening based on genomic and genetic
 CC techniques rather than on phenotypic observation. The method identifies
 CC and characterises genes via mutagenesis to identify genes encoding
 CC products which may have therapeutic benefit. The method also identifies
 CC the presence of mutations in a gene which do not rely solely upon prior
 CC matching of a gene with a disease. Heterozygotic organisms can also be
 CC screened to identify those carrying a mutation in a copy of a gene of
 CC interest even though the gene may be recessive and therefore causes no
 CC phenotypic alteration

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2005, 14:11:57 ; Search time 1612.98 Seconds
(without alignments)
6608.974 Million cell updates/sec

Title: US-09-887-941B-11

Perfect score: 220
Sequence: 1 cgcctctctctctctctt.....ccactcgcgcgcgcgcgcgcgc 220

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

GenBml:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_stg:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 20 | 9.1 | 38 | A67657 | A67657 Sequence 77 |
| 2 | 20 | 9.1 | 38 | AR089867 | AR089867 Sequence 77 |
| 3 | 20 | 9.1 | 40 | A67658 | A67658 Sequence 78 |
| 4 | 20 | 9.1 | 40 | AR089868 | AR089868 Sequence 78 |
| 5 | 16 | 7.3 | 21 | BD061402 | BD061402 Peptide h |
| 6 | 16 | 7.3 | 34 | AR036378 | AR036378 Sequence 41 |
| 7 | 16 | 7.3 | 34 | I72126 | I72126 Sequence 41 |
| 8 | 15 | 6.8 | 20 | AR231302 | AR231302 Sequence 41 |
| 9 | 15 | 6.8 | 22 | BD185757 | BD185757 Method an |
| 10 | 15 | 6.8 | 22 | AX463195 | AX463195 Sequence |
| 11 | 15 | 6.8 | 36 | AR007111 | AR007111 Sequence |
| 12 | 15 | 6.8 | 36 | AR013928 | AR013928 Sequence |
| 13 | 15 | 6.8 | 36 | E36400 | E36400 Peptide inh |
| 14 | 15 | 6.8 | 36 | I60579 | I60579 Sequence 30 |
| 15 | 15 | 6.8 | 36 | I70532 | I70532 Sequence 30 |
| 16 | 15 | 6.8 | 37 | AX803954 | AX803954 Sequence |
| 17 | 14 | 6.4 | 21 | A66714 | A66714 Sequence 9 |
| 18 | 14 | 6.4 | 21 | A66715 | A66715 Sequence 10 |
| 19 | 14 | 6.4 | 21 | AX009272 | AX009272 Sequence |

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|---|----|----|-----|----|---|----------|--------------------|
| c | 20 | 14 | 6.4 | 27 | 6 | AR143797 | AR143797 Sequence |
| c | 21 | 14 | 6.4 | 29 | 6 | I46792 | I46792 Sequence 12 |
| c | 22 | 14 | 6.4 | 30 | 6 | A76886 | A76886 Sequence 18 |
| c | 23 | 14 | 6.4 | 30 | 6 | AR151235 | AR151235 Sequence |
| | 24 | 14 | 6.4 | 33 | 6 | A29391 | A29391 degenerate |
| | 25 | 14 | 6.4 | 33 | 6 | A29394 | A29394 degenerate |
| | 26 | 14 | 6.4 | 33 | 6 | AR022452 | AR022452 Sequence |
| | 27 | 14 | 6.4 | 33 | 6 | AR022455 | AR022455 Sequence |
| | 28 | 14 | 6.4 | 33 | 6 | AR068930 | AR068930 Sequence |
| | 29 | 14 | 6.4 | 33 | 6 | AR068933 | AR068933 Sequence |
| | 30 | 14 | 6.4 | 33 | 6 | AR076577 | AR076577 Sequence |
| | 31 | 14 | 6.4 | 33 | 6 | AR134957 | AR134957 Sequence |
| | 32 | 14 | 6.4 | 33 | 6 | AR134960 | AR134960 Sequence |
| | 33 | 14 | 6.4 | 33 | 6 | AR141786 | AR141786 Sequence |
| | 34 | 14 | 6.4 | 33 | 6 | AR141789 | AR141789 Sequence |
| | 35 | 14 | 6.4 | 33 | 6 | AR143303 | AR143303 Sequence |
| | 36 | 14 | 6.4 | 33 | 6 | AR143306 | AR143306 Sequence |
| | 37 | 14 | 6.4 | 33 | 6 | AR151912 | AR151912 Sequence |
| | 38 | 14 | 6.4 | 33 | 6 | AR151915 | AR151915 Sequence |
| | 39 | 14 | 6.4 | 33 | 6 | I36392 | I36392 Sequence 90 |
| | 40 | 14 | 6.4 | 33 | 6 | I36395 | I36395 Sequence 93 |
| | 41 | 14 | 6.4 | 33 | 6 | I88092 | I88092 Sequence 90 |
| | 42 | 14 | 6.4 | 33 | 6 | I88095 | I88095 Sequence 93 |
| | 43 | 14 | 6.4 | 33 | 6 | AR226313 | AR226313 Sequence |
| | 44 | 14 | 6.4 | 33 | 6 | AR226316 | AR226316 Sequence |
| | 45 | 14 | 6.4 | 34 | 6 | A29393 | A29393 degenerate |

ALIGNMENTS

RESULT 1
LOCUS A67657 38 bp DNA linear PAT 05-MAY-1999
DEFINITION Sequence 77 from Patent WO9744485.
ACCESSION A67657
VERSION A67657.1 GI:4756520
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 38)
AUTHORS Goodfellow,P.N.
TITLE METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST
JOURNAL Patent: WO 9744485-A 77 27-NOV-1997;
HEXAGEN TECHNOLOGY LIMITED (GB)
FEATURES
source
1..38
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 9.1%; Score 20; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 50 GTCAACGCGAGTGAATCAG 69
Db 19 GTCAACGCGAGTGAATCAG 38

RESULT 2

LOCUS AR089867 38 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 149 from patent US 5994075.
ACCESSION AR089867
VERSION AR089867.1 GI:10016622
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)

AUTHORS Goodfellow,P.N.
TITLE Methods for identifying a mutation in a gene of interest without a phenotypic guide
JOURNAL Patent: US 5994075-A 149 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 9.1%; Score 20; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GTCACAGCGAGTGAATCAG 69
Db 19 GTCACAGCGAGTGAATCAG 38

RESULT 3
A67658/c 40 bp DNA linear PAT 05-MAY-1999
LOCUS A67658 Sequence 78 from Patent WO9744485.
ACCESSION A67658
VERSION A67658.1 GI:4756521
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 40)
AUTHORS Goodfellow,P.N.
TITLE METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST
JOURNAL Patent: WO 9744485-A 78 27-NOV-1997;
FEATURES HEXAGEN TECHNOLOGY LIMITED (GB)
source 1..40
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 9.1%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GACATTTCCCGAATTCGCA 179
Db 40 GACATTTCCCGAATTCGCA 21

RESULT 4
AR089868/c 40 bp DNA linear PAT 07-SEP-2000
LOCUS AR089868 Sequence 150 from patent US 5994075.
ACCESSION AR089868
VERSION AR089868.1 GI:10016623
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 40)
TITLE Goodfellow,P.N.
JOURNAL Methods for identifying a mutation in a gene of interest without a phenotypic guide
FEATURES Patent: US 5994075-A 150 30-NOV-1999;
source Location/Qualifiers
1..40
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 9.1%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GACATTTCCCGAATTCGCA 179
Db 40 GACATTTCCCGAATTCGCA 21

RESULT 5
BD061402/c 21 bp DNA linear PAT 27-AUG-2002
LOCUS BD061402 Peptide having a function regulating transcription of gene.
ACCESSION BD061402
VERSION BD061402.1 GI:22607008
KEYWORDS JP 2001292776-A/2.
SOURCE JP 2001292776-A/2.
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1 (bases 1 to 21)
AUTHORS Takagi,M., Shinji,H. and Ota,K.
TITLE Peptide having a function regulating transcription of gene
JOURNAL Patent: JP 2001292776-A 2 23-OCT-2001;
COMMENT AGENCY OF IND SCIENCE & TECHNOL
OS Artificial Sequence
PN JP 2001292776-A/2
PD 23-OCT-2001
PF 11-APR-2000 JP 2000109760
PI MASARU TAKAGI,HIDEAKI SHINJI,KEN OTA
PC C12N15/09,C07K14/415,C12N5/10//C12N15/09,C12R1.91,C12N15/00,
PC C12N5/00,C12R1.91
PC (C12N15/00,C12R1.91)
CC Description of Artificial Sequence: Synthetic primer DNA FH
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 7.3%; Score 16; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 CCTCTCCCTTTCCTCA 48
Db 18 CCTCTCCCTTTCCTCA 3

RESULT 6
AR036378 34 bp DNA linear PAT 29-SEP-1999
LOCUS AR036378 Sequence 41 from patent US 5872105.
ACCESSION AR036378
VERSION AR036378.1 GI:5953046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 34)
TITLE Kool,E.T.
JOURNAL Single-stranded circular oligonucleotides useful for drug delivery
FEATURES Patent: US 5872105-A 41 16-FEB-1999;
source Location/Qualifiers
1..34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 7.3%; Score 16; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTCTTTTCCCTTTC 29